

69. The method of claim 67, wherein the insect is selected from the group consisting of: *D. virgifera virgifera*; *D. virgifera zea*; *D. undecimpunctata*; *D. balteata*; *D. barberi*; and *D. speciosa*.

70. The method of claim 64, wherein target crop pest or pathogen is a nematode.

71. The method of claim 64, wherein the target crop pest or pathogen is a *Diabrotica* spp.

72. The method of claim 64, wherein the region comprises from about 19 bp to about 50 bp substantially complementary to a coding sequence of the target crop pest or pathogen.

73. The method of claim 72, wherein the region comprises from about 21 bp to about 30 bp substantially complementary to a coding sequence of the target crop pest or pathogen.

74. The method of claim 64, comprising identifying at least a second region within the starting molecule that when expressed as a dsRNA inhibits feeding by the target crop pest or pathogen or progeny thereof and linking the second region to the second nucleic acid molecule or a third nucleic acid molecule that when expressed as a dsRNA does not inhibit feeding by a target crop pest or pathogen or progeny thereof following uptake of the dsRNA expressed from the third nucleic acid molecule by the target plant pest or pathogen.

75. The method of claim 64, wherein the region is not substantially complementary to a nucleic acid of a non-target crop pest or pathogen.

76. The method of claim 64, wherein the region is complementary to a nucleic acid unique to the species in which the target crop pest or pathogen is classified.

77. The method of claim 64, wherein the region is complementary to a nucleic acid unique to the genus in which the target crop pest or pathogen is classified.

78. The method of claim 64, wherein the region is unique to *Diabrotica* spp.

79. The method of claim 78, wherein the region is unique to a *Diabrotica* spp. selected from the group consisting of *Diabrotica undecimpunctata howardii* (Southern Corn Rootworm (SCR)), *Diabrotica virgifera virgifera* (Western Corn Rootworm (WCR)), *Diabrotica barberi* (Northern Corn Rootworm (NCR)), *Diabrotica virgifera zea* (Mexican Corn Rootworm (MCR)), *Diabrotica balteata*, *Diabrotica viridula*, and *Diabrotica speciosa* (Brazilian Corn Rootworm (BZR)).

80. A method of controlling feeding by a target crop plant pest or pathogen or progeny thereof on a plant comprising introducing into the plant an expression construct prepared by the method of claim 64.

81. A dsRNA expressed by an expression construct prepared by the method of claim 64.

82. A plant cell transformed with an expression construct prepared by the method of claim 64.

83. A method of enhancing the control of a target crop pest or pathogen in a plant comprising expressing in the cells of the plant at least two dsRNA sequences that function upon uptake by the pest or pathogen to inhibit the expression of at least a first target coding sequence within the target crop pest or pathogen, wherein the two dsRNA sequences are substantially complementary to two non-contiguous portions of the first target coding sequence or to two different coding sequences of the target crop pest or pathogen.

84. The method of claim 83, wherein the two dsRNA sequences comprises about 19 bp to about 80 bp.

85. The method of claim 83, wherein the two dsRNA sequences comprises about 19 bp to about 50 bp.

86. The method of claim 83, wherein the two dsRNA sequences comprises about 21 bp to about 30 bp.

87. The method of claim 83, wherein the two dsRNA sequences are substantially complementary to at least two target coding sequences of the target crop pest or pathogen.

88. The method of claim 87, further comprising expressing in the cells of the plant at least a third dsRNA sequence that functions upon uptake by the pest or pathogen to inhibit the expression of a third target coding sequence within the target crop pest or pathogen, wherein the third dsRNA sequence is substantially complementary to a portion of the third target coding sequence.

89. The method of claim 83, wherein the two dsRNA sequences are expressed from regions selected from a starting nucleic acid molecule that when expressed as a dsRNA inhibits feeding by a target crop pest or pathogen or progeny thereof following uptake of the dsRNA by the target crop pest or pathogen.

90. The method of claim 89, wherein the starting nucleic acid molecule is a cDNA from the target crop pest or pathogen.

91. The method of claim 83, further comprising expressing a polynucleotide sequence in the cell selected from the group consisting of a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporus* insecticidal protein, and a *Bacillus sphaericus* insecticidal protein.

92. The method of claim 91, wherein the *Bacillus thuringiensis* insecticidal protein is selected from the group consisting of a Cry1, a Cry3, a TIC851, a CryET70, a Cry2, ET29, ET37, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, a binary insecticidal protein ET29 and TIC810, a binary insecticidal protein ET37 and TIC812, and a binary insecticidal protein PS149B1.

93. The method of claim 83, wherein the target coding sequence encodes a protein, the predicted function of which is selected from the group consisting of muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, digestive enzyme synthesis, maintenance of cell membrane potential, feeding site formation, feeding site development, feeding site maintenance, infection, molting, amino acid biosynthesis, amino acid degradation, sperm formation, pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation, development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, and apoptosis.

94. The method of claim 87, wherein the two target coding sequences perform at least two functions essential for target crop pest or pathogen survival that are suppressed by the dsRNA sequences, the functions being selected from the group consisting of feeding by the pest or pathogen, cell apoptosis, cell differentiation and development, capacity or desire for sexual reproduction, muscle formation, muscle twitching, muscle contraction, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation, phero-